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Data Paper

Exploring the taxonomic composition of two fungal communities on the Swedish west coast through metabarcoding

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Abstract

Background

Fungi are heterotrophic, unicellular or filamentous organisms that exhibit a wide range of different lifestyles as, e.g., symbionts, parasites, and saprotrophs. Mycologists have traditionally considered fungi to be a nearly exclusively terrestrial group of organisms, but it is now known that fungi have a significant presence in aquatic environments as well. We know little about most fungi in limnic and marine systems, including aspects of their taxonomy, ecology, and geographic distribution. The present study seeks to improve our knowledge of fungi in the marine environment. The fungal communities of two coastal marine environments of the Kattegat sea, Sweden, were explored with metabarcoding techniques using the nuclear ribosomal internal transcribed spacer 2 (ITS2) metabarcode. Our data add new information to the current picture of fungal community composition in benthic and coastal habitats in Northern Europe.

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New information

The dataset describes the number of operational taxonomic units (OTUs) and their taxonomic affiliations in two littoral gradients sampled on the Swedish west coast, Gothenburg municipality. Our data include basic diversity indices as well as chemical and edaphic sediment/soil parameters of the sampling sites. From the sites, 3470 and 4315 fungal OTUs, respectively, were recovered. The number of reads were 673,711 and 779,899, respectively, after quality filtering. Within the benthic sites, more than 80% of the sequences could not be classified taxonomically. The phylum composition of the classifiable sequences was dominated in both localities by Dikarya, which made up around 33% of the OTUs. Within Dikarya, Ascomycota was the dominant phylum. Guild assignment failed for more than half of the classifiable OTUs, with undefined saprotrophs being the most common resolved guild. This guild classification was slightly more common in the ocean sediment samples than in the terrestrial ones. Our metadata indicated that ocean sites contain organisms at a lower trophic level and that there are predominantly endophytic, parasitic, and pathogenic fungi in the marine environments. This hints at the presence of interesting and currently poorly understood fungus-driven ecological processes. It is also clear from our results that a very large number of marine fungi are in urgent need of taxonomic study and formal description.

Keywords

Biodiversity, Ecology, Marine fungi, Metabarcoding, High-throughput sequencing, Fungal diversity

Introduction

The fungal kingdom may hold as many as 3.8 million extant species, but only around 146,000 have been formally described so far (Hawksworth and Lücking 2017, Kirk 2019). Many fungi are inconspicuous with largely cryptic lifestyles, and many species from across the fungal tree of life do not seem to form conspicuous morphological structures such a fruiting bodies in any way that is currently appreciated (Tedersoo et al. 2017). Fungi take up dissolved carbonic matter by absorption and they interact with all major groups of organisms (Taylor et al. 2014); indeed, the fungal kingdom comprises organisms with a wide range of ecologically important lifestyles, including decomposers, parasites, pathogens, and symbionts/mutualists (Stajich et al. 2009). Fungi are traditionally thought of as terrestrial organisms, and the relatively few aquatic taxa known and studied in the pre-molecular era were largely associated with submerged terrestrial substrates such as driftwood and plant debris. Molecular studies have changed that by showing that fungi permeate not only terrestrial but also aquatic systems (Amend et al. 2019, Gladfelter et al. 2019). For instance, we now know that fungi are found throughout marine systems, from

the sediment through the water column to various associations with marine animals, plants, and algae (Jones and Pang 2012, Gnavi et al. 2014, Raghukumar 2017).

Although we are nowhere near a complete understanding of the ecological roles and taxonomic diversity of fungi in aquatic systems, data are starting to emerge. Recent results suggest that fungi degrade significant amounts of biomass in aquatic systems, just like they do on land, where biomass is degraded by fungal saprotrophs into simpler biomolecules that are subsequently absorbed (Raghukumar 2017). There is also evidence that the zoospores of chytrids are grazed by marine zooplankton, which has an impact on higher-level consumers in the marine trophic chain (Lepelletier et al. 2014). Other marine fungi are parasitic or pathogenic, thereby restructuring aquatic nutrient flows through processes such as the mycoloop (Kagami et al. 2014, Grossart et al. 2019). Fungi are, in other words, potentially able to structure and control the functioning of aquatic food webs (Jones 2011, Grossart et al. 2016).

Studying marine fungi through traditional lab and culture-based methods is a very slow and painstaking process, as many fungi are difficult to raise in culture (Stajich et al. 2009). This is particularly true for fungi that form associations with other organisms, such as endosymbionts and endoparasites. The marine environment adds another layer of complexity to cultivation efforts through aspects such as salt levels, pH, temperature, and light regimes. As an alternative to cultivation, environmental DNA of fungal communities is increasingly assessed by metabarcoding, a biodiversity assessment method that combines DNA-based identification and high-throughput (HTS) DNA sequencing (Nilsson et al. 2019a). Metabarcoding can be used to characterise entire fungal communities using a relatively short DNA barcode, such as the internal transcribed spacer region (ITS) of the nuclear ribosomal DNA operon (Schoch et al. 2012). Barcode amplification relies on taxon-specific primers that ideally target all fungi. Ill-chosen primers will lead to biases in terms of what taxa are recovered, masking environmental signals and distorting the view of the fungal communities obtained (Ihrmark et al. 2012, Tedersoo et al. 2015). What species and what taxonomic levels are recovered is also dependent on the completeness of the reference databases for fungi, the most complete and up-to-date one being UNITE (Nilsson et al. 2019b).

Numerous studies over the last decade have sought to assess the fungal biodiversity in different local areas and habitats (Hiiesalu et al. 2014, Urbina et al. 2016, Pec et al. 2017) as well as globally (Tedersoo et al. 2014, Davison et al. 2015). A fair number of studies have examined terrestrial fungal diversity in Sweden (Lindahl et al. 2007, Ihrmark et al. 2012, Varenius et al. 2016), but studies of marine fungi in Sweden are much more rare (Eriksson 2014, Tibell 2016, Tibell et al. 2019). The purpose of this study was to investigate how well fungal taxa collected from coastal sediments of the Kattegat sea in western Sweden have been documented so far. As in many other areas, waters in the Kattegat sea have been impacted by anthropogenic pressures such as eutrophication and fisheries (Josefson et al. 2018). To be able to track future changes in fungal diversity and abundance, it is important to generate baseline datasets. With this dataset, we seek to add to the taxonomic and ecological knowledge of marine fungal communities through ITS2-based metabarcoding of two coastal localities on the Swedish west coast.

Project description

Study area description: We targeted two different localities of similar ecology and habitat. The first sampling was carried out at Askimsbadet, Gothenburg Municipality, Västra Götalands county (Fig. 1). This locality is characterized by a shallow saltwater bay with a short intertidal shoreline and a sandy beach becoming meadow-like with high grass and reeds. The second sampling was undertaken on the island Stora Amundön, Gothenburg Municipality, Västra Götalands county (Fig. 2). It consisted of a shallow sandy cove turning into a grassy meadow landscape. The grassland was surrounded by rocks and shrubs and was replaced by mixed woodland after a stretch of around 60 m. Both transects were approximately 160 m long. The geographic coordinates and altitude of each sampling area were recorded, and the ectomycorrhizal plant cover at each site was noted. Sampling sites are numbered according to Figs 1, 2 and are indicated by parentheses in the following plant cover description. The vegetation at the Askimsbadet site consisted of mostly dried seaweed at the shoreline, but gradually turned into a natural reed and grass landscape after around 3 m, with a few grazing plants such as *Lysimachia maritima* and *Argentina anserina* (7). These plants, along with *Rumex* sp. and *Anthriscus sylvestris*, could also be found further up in the meadow landscape (6, 5). They were later replaced by *Taraxacum* sp., *Cirsium* sp. (4, 1), and *Urtica* sp. (3), although *Anthriscus sylvestris* and *Rumex* sp. could be found all along the gradient. The furthest up, genera and species such as *Equisetum* sp., *Taxus* sp., *Thuja* sp., *Malus* sp., *Rubus* sp., and *Calystegia sepium* could be spotted (1). The vegetation at the Stora Amundön site consisted of dried seaweed at the shoreline (7) that was replaced by a mown grass landscape (6, 5, 4) where *Erica* sp., *Taraxacum* sp., *Juniperus* sp. (5), and young *Quercus* sp. (4) could be found. Further up, the landscape transformed into a mixture of deciduous and coniferous forest that consisted of *Quercus* sp., *Juniperus* sp., *Populus* sp., *Betula* sp., *Pinus* sp. (1, 2, 3), and some fern taxa such as *Pteridium* sp. (3) and *Polypodium vulgare* (2).

Sampling methods

Sampling description: We followed the soil sampling protocol of Tedersoo et al. (2014) with some slight adaptations to assess a spatial gradient from land through an intertidal shoreline into the ocean. Additionally, pH and salinity were measured at all sampling points. At each of the two localities, soil was collected along the transect, which was sampled every 20 meters, resulting in nine different sampling sites (Figs 1, 2). Of those nine sites, six were located within the meadow or forest stretch, respectively, and were approximately at sea-level, one site was located on the shoreline, and two were sampled from the seabed at approximately 1 to 2 m below the ocean surface. For both transects, the following procedure was adopted. Two samples were taken from each site and diluted 1:1 with freshwater to measure the pH and conductivity of the soil/sediment. The average of these two measurements was used as an estimate of the true values. At each site, 10 replicate cores were sampled with a metal bulb planter, all within a radius of 20 m. Each core consisted of the top 5 cm of soil/sediment and had a diameter of 5 cm. Where